T. Prasthoter
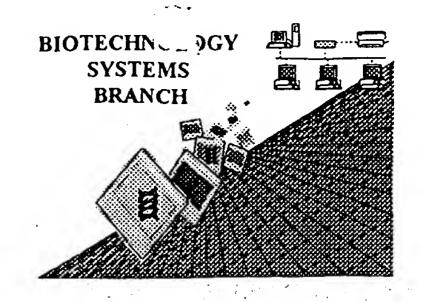
RAW SEQUENCE LISTING ERROR REPORT

#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/429,798_

Source: _1627_

Date Processed by STIC: _4-17-01_

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2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING   DATE: 04/17/2001
PATENT APPLICATION: US/09/429,798   TIME: 13:01:22

    Input Set : A:\9233-8DV1.txt
    Output Set: N:\CRF3\04172001\I429798.raw

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 3 <110> APPLICANT: Ekwuribe, Nnochiri
 4          Radhakrishnan, Balasingam
 5          Price, Christopher
 6          Anderson, Wesley
 7          Ansari, Aslam
 9 <120> TITLE OF INVENTION: BLOOD-BRAIN BARRIER THERAPEUTICS
11 <130> FILE REFERENCE: 9233.8DV1
13 <140> CURRENT APPLICATION NUMBER: 09/429,798
14 <141> CURRENT FILING DATE: 1999-10-29
16 <150> PRIOR APPLICATION NUMBER: 09/134,803
17 <151> PRIOR FILING DATE: 1998-08-14
19 <160> NUMBER OF SEQ ID NOS: 52
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6
25 <212> TYPE: PRT
26 <213> ORGANISM: synthetic construct
28 <220> FEATURE:
29 <221> NAME/KEY: MOD_RES
30 <222> LOCATION: (6)..(6)
31 <223> OTHER INFORMATION: Polymer connected to epsilon-amino group
34 <400> SEQUENCE: 1
36 Tyr Gly Gly Phe Met Lys
37 1               5
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 6
41 <212> TYPE: PRT
42 <213> ORGANISM: synthetic construct
44 <220> FEATURE:
45 <221> NAME/KEY: MOD_RES
46 <222> LOCATION: (1)..(1)
47 <223> OTHER INFORMATION: Polymer connected to alpha-amino group
50 <220> FEATURE:
51 <221> NAME/KEY: MOD_RES
52 <222> LOCATION: (6)..(6)
53 <223> OTHER INFORMATION: Polymer connected to epsilon-amino group
56 <400> SEQUENCE: 2
58 Tyr Gly Gly Phe Met Lys
59 1               5
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 6
63 <212> TYPE: PRT
64 <213> ORGANISM: synthetic construct
66 <220> FEATURE:
67 <221> NAME/KEY: MOD_RES
68 <222> LOCATION: (1)..(1)
69 <223> OTHER INFORMATION: Polymer connected to alpha-amino group
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/429,798

DATE: 04/17/2001
TIME: 13:01:22

Input Set : A:\9233-8DV1.txt
Output Set: N:\CRF3\04172001\I429798.raw

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 74 Tyr Gly Gly Phe Met Lys
 75 1               5
 77 <210> SEQ ID NO: 4
 78 <211> LENGTH: 6
 79 <212> TYPE: PRT
 80 <213> ORGANISM: synthetic construct
 82 <220> FEATURE:
 83 <221> NAME/KEY: MOD_RES
 84 <222> LOCATION: (1)..(1)
 85 <223> OTHER INFORMATION: ACETYLATION
 88 <220> FEATURE:
 89 <221> NAME/KEY: MOD_RES
 90 <222> LOCATION: (6)..(6)
 91 <223> OTHER INFORMATION: AMIDATION
 94 <400> SEQUENCE: 4
 96 Phe Arg Trp Trp Tyr Lys
 97 1               5
 99 <210> SEQ ID NO: 5
100 <211> LENGTH: 6
101 <212> TYPE: PRT
102 <213> ORGANISM: synthetic construct
104 <220> FEATURE:
105 <221> NAME/KEY: MOD_RES
106 <222> LOCATION: (1)..(1)
107 <223> OTHER INFORMATION: ACETYLATION
110 <220> FEATURE:
111 <221> NAME/KEY: MOD_RES
112 <222> LOCATION: (6)..(6)
113 <223> OTHER INFORMATION: AMIDATION
116 <400> SEQUENCE: 5
118 Arg Trp Ile Gly Trp Lys
119 1               5
121 <210> SEQ ID NO: 6
122 <211> LENGTH: 6
123 <212> TYPE: PRT
124 <213> ORGANISM: synthetic construct
126 <220> FEATURE:
127 <221> NAME/KEY: MOD_RES
128 <222> LOCATION: (6)..(6)
129 <223> OTHER INFORMATION: AMIDATION
132 <220> FEATURE:
133 <221> NAME/KEY: UNSURE
134 <222> LOCATION: (6)..(6)/
135 <223> OTHER INFORMATION: Xaa can be any of the twenty naturally occurring amino acids
138 <400> SEQUENCE: 6
140 Trp Trp Pro Lys His Xaa
141 1               5
143 <210> SEQ ID NO: 7
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W--> (line 140)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/429,798

DATE: 04/17/2001
TIME: 13:01:22

Input Set : A:\9233-8DV1.txt
Output Set: N:\CRF3\04172001\I429798.raw

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144 <211> LENGTH: 4
145 <212> TYPE: PRT
146 <213> ORGANISM: synthetic construct
148 <220> FEATURE:
149 <221> NAME/KEY: MOD_RES
150 <222> LOCATION: (4)..(4)
151 <223> OTHER INFORMATION: AMIDATION
154 <220> FEATURE:
155 <221> NAME/KEY: UNSURE
156 <222> LOCATION: (4)..(4)  /
157 <223> OTHER INFORMATION: Xaa is either Lys or Arg
160 <400> SEQUENCE: 7
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W--> 162 Trp Trp Pro Xaa
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163 1
165 <210> SEQ ID NO: 8
166 <211> LENGTH: 6
167 <212> TYPE: PRT
168 <213> ORGANISM: synthetic construct
170 <220> FEATURE:
171 <221> NAME/KEY: MOD_RES
172 <222> LOCATION: (6)..(6)
173 <223> OTHER INFORMATION: AMIDATION
176 <220> FEATURE:
177 <221> NAME/KEY: UNSURE
178 <222> LOCATION: (6)..(6) /
179 <223> OTHER INFORMATION: Xaa can be any one of the naturally occurring amino acids
182 <400> SEQUENCE: 8
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W--> 184 Tyr Pro Phe Gly Phe Xaa
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185 1                 5
187 <210> SEQ ID NO: 9
188 <211> LENGTH: 7
189 <212> TYPE: PRT
190 <213> ORGANISM: synthetic construct
192 <220> FEATURE:
193 <221> NAME/KEY: MOD_RES
194 <222> LOCATION: (1)..(5)
195 <223> OTHER INFORMATION: Amino acids are in the D-form
198 <220> FEATURE:
199 <221> NAME/KEY: MOD_RES
200 <222> LOCATION: (6)..(6)
201 <223> OTHER INFORMATION: n is 0 or 1
204 <220> FEATURE:
205 <221> NAME/KEY: MOD_RES
206 <222> LOCATION: (7)..(7)  /
207 <223> OTHER INFORMATION: Xaa is Gly or the D-form of a naturally occurring amino acid
210 <220> FEATURE:
211 <221> NAME/KEY: MOD_RES
212 <222> LOCATION: (7)..(7)
213 <223> OTHER INFORMATION: AMIDATION
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        216 <400> SEQUENCE: 9
W--> 218 Ile Met Ser Trp Trp Gly Xaa
        219 1               5
        221 <210> SEQ ID NO: 10
        222 <211> LENGTH: 6
        223 <212> TYPE: PRT
        224 <213> ORGANISM: synthetic construct
        226 <220> FEATURE:
        227 <221> NAME/KEY: MOD_RES
        228 <222> LOCATION: (1)..(4)
        229 <223> OTHER INFORMATION: Amino acids are in the D-form
        232 <220> FEATURE:
        233 <221> NAME/KEY: MOD_RES
        234 <222> LOCATION: (6)..(6)
        235 <223> OTHER INFORMATION: Xaa is Gly or the D-form of a naturally-occurring amino acid
        238 <220> FEATURE:
        239 <221> NAME/KEY: MOD_RES
        240 <222> LOCATION: (6)..(6)
        241 <223> OTHER INFORMATION: AMIDATION
        244 <400> SEQUENCE: 10
W--> 246 Ile Met Thr Trp Gly Xaa
        247 1               5
        249 <210> SEQ ID NO: 11
        250 <211> LENGTH: 4
        251 <212> TYPE: PRT
        252 <213> ORGANISM: synthetic construct
        254 <220> FEATURE:
        255 <221> NAME/KEY: MOD_RES
        256 <222> LOCATION: (2)..(2)
        257 <223> OTHER INFORMATION: Xaa is A1, wherein A1 is the D-form of Nve or Nle
        260 <220> FEATURE:
        261 <221> NAME/KEY: MOD_RES
        262 <222> LOCATION: (3)..(3)
        263 <223> OTHER INFORMATION: Xaa is B2, wherein B2 is Gly, Phe, or Trp
        266 <220> FEATURE:
        267 <221> NAME/KEY: MOD_RES
        268 <222> LOCATION: (4)..(4)
        269 <223> OTHER INFORMATION: Xaa is C3, wherein C3 is Trp or Nap
        272 <220> FEATURE:
        273 <221> NAME/KEY: MOD_RES
        274 <222> LOCATION: (4)..(4)
        275 <223> OTHER INFORMATION: AMIDATION
        278 <400> SEQUENCE: 11
W--> 280 Tyr Xaa Xaa Xaa
        281 1
        283 <210> SEQ ID NO: 12
        284 <211> LENGTH: 3
        285 <212> TYPE: PRT
        286 <213> ORGANISM: synthetic construct
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RAW SEQUENCE LISTING   DATE: 04/17/2001
PATENT APPLICATION: US/09/429,798   TIME: 13:01:22

Input Set : A:\9233-8DV1.txt
Output Set: N:\CRF3\04172001\I429798.raw

```
288 <220> FEATURE:
289 <221> NAME/KEY: MOD_RES
290 <222> LOCATION: (1)..(1)
291 <223> OTHER INFORMATION: Tyr has at its N-terminus an Me-x-H-y-N group, wherein x is 0, 1,
292       or 2; and y is 0, 1, or 2, with the proviso that x and y is neve
293       r greater than ____     ? incomplete explaination.
296 <220> FEATURE:
297 <221> NAME/KEY: MOD_RES
298 <222> LOCATION: (1)..(2)
299 <223> OTHER INFORMATION: The amine between the first Tyr and the second Tyr is methylated
303 <220> FEATURE:
304 <221> NAME/KEY: MOD_RES
305 <222> LOCATION: (3)..(3)
306 <223> OTHER INFORMATION: Xaa is Xaa-z, wherein Xaa is Phe, (D)Phe, or NHBzl, and wherein z
307       is 0 or ____        ? incomplete explanation
310 <220> FEATURE:
311 <221> NAME/KEY: MOD_RES
312 <222> LOCATION: (3)..(3)
313 <223> OTHER INFORMATION: AMIDATION
316 <400> SEQUENCE: 12
318 Tyr Tyr Xaa        W-->
319 1
321 <210> SEQ ID NO: 13
322 <211> LENGTH: 6
323 <212> TYPE: PRT
324 <213> ORGANISM: synthetic construct
326 <220> FEATURE:
327 <221> NAME/KEY: MOD_RES
328 <222> LOCATION: (4)..(4) /
329 <223> OTHER INFORMATION: Xaa is D4, wherein D4 is Lys or Arg
332 <220> FEATURE:
333 <221> NAME/KEY: MOD_RES
334 <222> LOCATION: (5)..(5)
335 <223> OTHER INFORMATION: His is His-z, wherein z is 0 or 1
338 <220> FEATURE:
339 <221> NAME/KEY: MOD_RES
340 <222> LOCATION: (6)..(6)
341 <223> OTHER INFORMATION: Xaa is Xaa-z, wherein Xaa is a naturally occurring amino acid and
342       z is 0 or ____      ? incomplete explaination
345 <220> FEATURE:
346 <221> NAME/KEY: MOD_RES
347 <222> LOCATION: (6)..(6)
348 <223> OTHER INFORMATION: AMIDATION
351 <400> SEQUENCE: 13
353 Trp Trp Pro Xaa His Xaa      W-->
354 1               5
356 <210> SEQ ID NO: 14
357 <211> LENGTH: 4
358 <212> TYPE: PRT
```

F.Y.I.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.